

F. Moezie

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/068,253

DATE: 04/20/2001
TIME: 12:57:28

Input Set : A:\19624051.app
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ENTERED

3 <110> APPLICANT: SHIMURA, Takesada
4 TORIYAMA, Satsuki
6 <120> TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
8 <130> FILE REFERENCE: 146.1286
10 <140> CURRENT APPLICATION NUMBER: 09/068,253
11 <141> CURRENT FILING DATE: 1998-06-09
13 <150> PRIOR APPLICATION NUMBER: PCT/JP96/03333
14 <151> PRIOR FILING DATE: 1996-11-14
16 <150> PRIOR APPLICATION NUMBER: JP 7/322402
17 <151> PRIOR FILING DATE: 1995-11-17
19 <160> NUMBER OF SEQ ID NOS: 4
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 357
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(357)
31 <223> OTHER INFORMATION: Relevant amino acid residues in SEQ ID NO: 1 from
32 1 to 119 in WO 95/04819
34 <300> PUBLICATION INFORMATION:
35 <301> AUTHORS: HOTTEN, Gertrud
36 NEIDHARDT, Helge
37 PAULISTA, Michael
38 <302> TITLE: NEW GROWTH/DIFFERENTIATION FACTOR OF THE TGF-BETA
39 FAMILY
40 <310> PATENT DOC NO: WO 95/04819
41 <311> PATENT FILING DATE: 1995-02-16
42 <313> RELEVANT RESIDUES: 1 TO 119
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45 cca ctg gcc act cgc cag ggc aag cga ccc agc aag aac ctt aag gct 48
46 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
47 1 5 10 15
49 cgc tgc agt cgg aag gca ctg cat gtc aac ttc aag gac atg ggc tgg 96
50 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
51 20 25 30
53 gac gac tgg atc atc gca ccc ctt gag tac gag gct ttc cac tgc gag 144
54 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
55 35 40 45
57 ggg ctg tgc gag ttc cca ttg cgc tcc cac ctg gag ccc acg aat cat 192
58 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
59 50 55 60
61 gca gtc atc cag acc ctg atg aac tcc atg gac ccc gag tcc aca cca 240
62 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
63 65 70 75 80
65 ccc acc tgc tgt gtg ccc acg cga ctg agt ccc atc agc atc ctc ttc 288

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66 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
67      85      90      95
69 att gac tct gcc aac aac gtg gtg tat aag cag tat gag gac atg gtc 336
70 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
71      100      105      110
73 gtg gag tcg tgt gcc tgc agg 357
74 Val Glu Ser Cys Gly Cys Arg
75      115
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 119
80 <212> TYPE: PRT
81 <213> ORGANISM: Homo sapiens
83 <400> SEQUENCE: 2
84 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
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87 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
88      20      25      30
90 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
91      35      40      45
93 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
94      50      55      60
96 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
97      65      70      75      80
99 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
100      85      90      95
102 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
103      100      105      110
105 Val Glu Ser Cys Gly Cys Arg
106      115
110 <210> SEQ ID NO: 3
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116 <223> OTHER INFORMATION: Description of Artificial Sequence:
117      oligonucleotide
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120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(27)
122 <223> OTHER INFORMATION: PCR forward primer for isolating mature-type MP52
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128 <210> SEQ ID NO: 4
129 <211> LENGTH: 26
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence:
135      oligonucleotide

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137 <220> FEATURE:

138 <221> NAME/KEY: misc_feature

139 <222> LOCATION: Complement((1)..(26))

140 <223> OTHER INFORMATION: PCR reverse primer for isolating mature-type MP52

142 <400> SEQUENCE: 4

143 cgtcgactac ctgcagccac acgact

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VERIFICATION SUMMARY

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